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Sequence Listing was accepted.

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Reviewer: Anne Corrigan

Timestamp: [year=2010; month=1; day=22; hr=8; min=18; sec=15; ms=873; ]

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Application No: 10587956 Version No: 2.0

**Input Set:**

**Output Set:**

**Started:** 2010-01-06 16:58:26.791  
**Finished:** 2010-01-06 16:58:28.474  
**Elapsed:** 0 hr(s) 0 min(s) 1 sec(s) 683 ms  
**Total Warnings:** 15  
**Total Errors:** 0  
**No. of SeqIDs Defined:** 19  
**Actual SeqID Count:** 19

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W 402	Undefined organism found in <213> in SEQ ID (2)
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W 213	Artificial or Unknown found in <213> in SEQ ID (14)
W 402	Undefined organism found in <213> in SEQ ID (15)

SEQUENCE LISTING

<110> Korea Research Institute of Bioscience and Biotechnology  
Kang, Hyun-As  
Kim, Moo-Woong  
Rhee, Sang-Ki  
Heo, Joo Hyung

<120> Novel Hansenula Polymorpha Gene Coding for Alpha  
1,6-Mannosyltransferase and Process for the Production of  
Recombinant Glycoproteins with Hansenula Polymorpha Mutant Strain  
Deficient in the Same Gene

<130> HANOL-13037

<140> 10587956  
<141> 2010-01-06

<150> PCT/KR 2004/001819  
<151> 2004-07-21

<150> KR 10-2004-0006352  
<151> 2004-01-30

<160> 19

<170> PatentIn version 3.5

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<213> Hansenula polymorpha

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<221> CDS  
<222> (10)..(1293)

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gtg ctg aag cgc gcg cga ctc tac atg gcg acg aat cgc cgg ctg gtg 99  
Val Leu Lys Arg Ala Arg Leu Tyr Met Ala Thr Asn Arg Arg Leu Val  
15 20 25 30

gtt gtt ctt gtg gtg ctg ctg tac tgg gtg gtc cag aac gtt tgg acg 147  
Val Val Leu Val Val Leu Tyr Trp Val Val Gln Asn Val Trp Thr  
35 40 45

tgg agc cct ggg acg cgc gat ttg gcc caa gtg gac gcg aag atc gag 195  
Trp Ser Pro Gly Thr Arg Asp Leu Ala Gln Val Asp Ala Lys Ile Glu  
50 55 60

gcc gag cta aac tcg aat cta cat act ttt gga gcg cat ttg cgc cac 243

Ala Glu Leu Asn Ser Asn Leu His Thr Phe Gly Ala His Leu Arg His			
65	70	75	
tta aac cgg ctt ccg gca gag tcg gcc acc ctg cgt gaa aaa ctc acc			291
Leu Asn Arg Leu Pro Ala Glu Ser Ala Thr Leu Arg Glu Lys Leu Thr			
80	85	90	
ttc tat ttc cca tat tat cct gaa aag ccc gtg ccg aac cag atc tgg			339
Phe Tyr Phe Pro Tyr Tyr Pro Glu Lys Pro Val Pro Asn Gln Ile Trp			
95	100	105	110
cag aca tgg aag gtc gat ctc gaa gac gac aac ttc ccc aag cag tac			387
Gln Thr Trp Lys Val Asp Leu Glu Asp Asp Asn Phe Pro Lys Gln Tyr			
115	120	125	
aga cgg ttt cag aag acg tgg gtc gag aaa aat cca gac tac gtg tac			435
Arg Arg Phe Gln Lys Thr Trp Val Glu Lys Asn Pro Asp Tyr Val Tyr			
130	135	140	
cac ctg att ccg gac tct gtg att gag gac ttt gtg gcg agt ttg tac			483
His Leu Ile Pro Asp Ser Val Ile Glu Asp Phe Val Ala Ser Leu Tyr			
145	150	155	
gcg aac gtg ccg gag gtg gtc aga gcg tac cag ctg ctt ccg aaa aat			531
Ala Asn Val Pro Glu Val Val Arg Ala Tyr Gln Leu Leu Pro Lys Asn			
160	165	170	
atc atg aag gcg gat ttt ttc cgg tat ttg gtg atc tac gcg cgc gga			579
Ile Met Lys Ala Asp Phe Phe Arg Tyr Leu Val Ile Tyr Ala Arg Gly			
175	180	185	190
ggc acc tac tca gac atg gac acg gtg tgt tta aag ccg atc aag gac			627
Gly Thr Tyr Ser Asp Met Asp Thr Val Cys Leu Lys Pro Ile Lys Asp			
195	200	205	
tgg gcc acg ttt gat cgc gac ctg atc cac gct gcc gac aat aag gcc			675
Trp Ala Thr Phe Asp Arg Asp Leu Ile His Ala Ala Asp Asn Lys Ala			
210	215	220	
gat ctc tcc cag ata gat cca gaa gca aga acc acg cct gtg ggg ctg			723
Asp Leu Ser Gln Ile Asp Pro Glu Ala Arg Thr Thr Pro Val Gly Leu			
225	230	235	
gtg att ggc att gag gcc gac ccg gac agg ccc gac tgg cac gag tgg			771
Val Ile Gly Ile Glu Ala Asp Pro Asp Arg Pro Asp Trp His Glu Trp			
240	245	250	
ttc tcg cgc aga ctg cag ttc tgc cag tgg acg atc cag gcg aag ccg			819
Phe Ser Arg Arg Leu Gln Phe Cys Gln Trp Thr Ile Gln Ala Lys Pro			
255	260	265	270
gga cac ccg ctg ctg cgc gag ctg atc atc cgg atc gtg gag gag acg			867
Gly His Pro Leu Leu Arg Glu Leu Ile Ile Arg Ile Val Glu Glu Thr			
275	280	285	
ttc cgc aaa cag cac atg ggc gtt ttg aaa aga gtg gaa ggc aag gac			915
Phe Arg Lys Gln His Met Gly Val Leu Lys Arg Val Glu Gly Lys Asp			

290	295	300	
tcg ggc gca gat atc atg cag tgg aca gga ccg ggg ata ttt aca gac Ser Gly Ala Asp Ile Met Gln Trp Thr Gly Pro Gly Ile Phe Thr Asp			963
305	310	315	
act ctg ttt gat tat ctg aac aat gtg gcg agc gac ggc aag ttg ggc Thr Leu Phe Asp Tyr Leu Asn Asn Val Ala Ser Asp Gly Lys Leu Gly			1011
320	325	330	
gac ggg tac ggc gtg ggg tcg ttg tat tgg cgc aag cac ggc aaa tat Asp Gly Tyr Gly Val Gly Ser Leu Tyr Trp Arg Lys His Gly Lys Tyr			1059
335	340	345	350
aag ctg aaa aag aca gaa att aac aag aat aac gag cca ttg cat tct Lys Leu Lys Lys Thr Glu Ile Asn Lys Asn Asn Glu Pro Leu His Ser			1107
355	360	365	
gag gac cag ctt atc aac tgg agg tcg ctg acc aac atg gac aag cca Glu Asp Gln Leu Ile Asn Trp Arg Ser Leu Thr Asn Met Asp Lys Pro			1155
370	375	380	
aag atc atg ggg gac gta atg gtg tta cca atc acg agc ttt agt ccg Lys Ile Met Gly Asp Val Met Val Leu Pro Ile Thr Ser Phe Ser Pro			1203
385	390	395	
aac gtg ggg cac atg ggc tca aag agc agc tca gat agg ctg gca ttt Asn Val Gly His Met Gly Ser Lys Ser Ser Ser Asp Arg Leu Ala Phe			1251
400	405	410	
gtg gag cat tta ttt tct ggc agc tgg aag cca aaa aac aaa Val Glu His Leu Phe Ser Gly Ser Trp Lys Pro Lys Asn Lys			1293
415	420	425	
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Leu Val Val Leu Leu Tyr Trp Val Val Gln Asn Val Trp Thr Trp Ser			
35	40	45	
Pro Gly Thr Arg Asp Leu Ala Gln Val Asp Ala Lys Ile Glu Ala Glu			

50

55

60

Leu Asn Ser Asn Leu His Thr Phe Gly Ala His Leu Arg His Leu Asn  
65 70 75 80

Arg Leu Pro Ala Glu Ser Ala Thr Leu Arg Glu Lys Leu Thr Phe Tyr  
85 90 95

Phe Pro Tyr Tyr Pro Glu Lys Pro Val Pro Asn Gln Ile Trp Gln Thr  
100 105 110

Trp Lys Val Asp Leu Glu Asp Asp Asn Phe Pro Lys Gln Tyr Arg Arg  
115 120 125

Phe Gln Lys Thr Trp Val Glu Lys Asn Pro Asp Tyr Val Tyr His Leu  
130 135 140

Ile Pro Asp Ser Val Ile Glu Asp Phe Val Ala Ser Leu Tyr Ala Asn  
145 150 155 160

Val Pro Glu Val Val Arg Ala Tyr Gln Leu Leu Pro Lys Asn Ile Met  
165 170 175

Lys Ala Asp Phe Phe Arg Tyr Leu Val Ile Tyr Ala Arg Gly Gly Thr  
180 185 190

Tyr Ser Asp Met Asp Thr Val Cys Leu Lys Pro Ile Lys Asp Trp Ala  
195 200 205

Thr Phe Asp Arg Asp Leu Ile His Ala Ala Asp Asn Lys Ala Asp Leu  
210 215 220

Ser Gln Ile Asp Pro Glu Ala Arg Thr Thr Pro Val Gly Leu Val Ile  
225 230 235 240

Gly Ile Glu Ala Asp Pro Asp Arg Pro Asp Trp His Glu Trp Phe Ser  
245 250 255

Arg Arg Leu Gln Phe Cys Gln Trp Thr Ile Gln Ala Lys Pro Gly His  
260 265 270

Pro Leu Leu Arg Glu Leu Ile Ile Arg Ile Val Glu Glu Thr Phe Arg  
275 280 285

Lys Gln His Met Gly Val Leu Lys Arg Val Glu Gly Lys Asp Ser Gly  
290 295 300

Ala Asp Ile Met Gln Trp Thr Gly Pro Gly Ile Phe Thr Asp Thr Leu  
305 310 315 320

Phe Asp Tyr Leu Asn Asn Val Ala Ser Asp Gly Lys Leu Gly Asp Gly  
325 330 335

Tyr Gly Val Gly Ser Leu Tyr Trp Arg Lys His Gly Lys Tyr Lys Leu  
340 345 350

Lys Lys Thr Glu Ile Asn Lys Asn Asn Glu Pro Leu His Ser Glu Asp  
355 360 365

Gln Leu Ile Asn Trp Arg Ser Leu Thr Asn Met Asp Lys Pro Lys Ile  
370 375 380

Met Gly Asp Val Met Val Leu Pro Ile Thr Ser Phe Ser Pro Asn Val  
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Gly His Met Gly Ser Lys Ser Ser Asp Arg Leu Ala Phe Val Glu  
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35 40 45

Lys Ile Val Ser Glu Tyr Leu Asn Asn Phe Tyr Lys Leu Asn Pro Lys  
50 55 60

Phe Arg Gly Ala Asn Pro Tyr Asp Ala Ala Val Thr Ala Glu Arg Leu  
65 70 75 80

Ala Lys Phe Phe Pro Tyr Asp Asn Ser Ala Arg Arg Ile Glu Lys Ser  
85 90 95

Ile Trp Gln Met Trp Lys Val Pro Ser Thr Asp Pro Asp Phe Pro His  
100 105 110

Lys Glu Leu Val Asn Lys Trp Lys Asn Glu Asn Pro Thr Tyr Lys Tyr  
115 120 125

Asn Leu Leu Thr Asp Asp Glu Ile Leu Glu Ile Leu Arg Ile Arg Phe  
130 135 140

Lys Asp Thr Val Pro Glu Val Leu Glu Ala Phe Glu Met Leu Pro Asn

145

150

155

160

Lys Ile Ile Arg Ser Asp Phe Ala Arg Tyr Leu Leu Ile Phe Leu Asn  
165 170 175

Gly Gly Val Tyr Ala Asp Ile Asp Thr Asp Leu Gln Lys Pro Val Asp  
180 185 190

Thr Trp Phe Asp Ser Asp Arg Asn Val Gly Phe Val Val Ala Val Glu  
195 200 205

Glu Asp Ile Asn Val Glu Asn Trp Glu His Tyr Met Thr Arg Arg Ile  
210 215 220

Gln Phe Glu Gln Trp Thr Phe Lys Ala Lys Ala Lys His Pro Ile Leu  
225 230 235 240

Arg Lys Leu Ile Ala Lys Ile Val Glu Thr Thr Phe Gln Ala Lys Lys  
245 250 255

Asn Asp Lys Leu Gln Ala Tyr Tyr Lys Asp Phe Lys Gly Val Asp Arg  
260 265 270

Cys Ala Ser Val Asp Ile Met Val Trp Thr Gly Pro Val Val Trp Thr  
275 280 285

Asp Thr Ile Tyr Ala His Leu Asn Ser Ile Pro Ser Pro Thr Ile Val  
290 295 300

Asp Ile Asp His Gln Arg Asp Ile Ala Gly Glu Leu Tyr Gly Pro Glu  
305 310 315 320

Thr Gly Glu Gly Asp Val Ile Ser Trp Arg Phe Phe Ala Gly Leu Arg  
325 330 335

Ala Pro Val Met Ile Asp Asp Val Val Ile Tyr Pro Arg Ala Ser Phe  
340 345 350

Arg Glu Asp Lys Glu Asn Asn Cys Gly Lys Tyr Cys Tyr Val His His  
355 360 365

His Phe Gly Gly Ser Trp Lys Asn Asn Gly Lys Gly Glu Ile Lys Pro  
370 375 380

Gly Met Glu Gly Tyr Glu Gly Glu Asp Pro Asn Glu Val Glu Glu Leu  
385 390 395 400

Arg Lys Asn Asp Val Ser Lys Arg Asp Val Ile Pro Gly Glu Ser Lys  
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Asp Val Ala Pro Val Lys Lys Leu Ala Lys Arg Cys Ala Tyr Pro Tyr  
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Thr Pro Tyr  
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Ser Leu Ser Ser Pro Thr Ser Thr His Lys Thr Glu Tyr Asn Ser Pro  
35 40 45

Lys Leu Gln Leu Ala Lys Glu Leu Glu Leu Asn Ser Asn Trp Lys Glu  
50 55 60

Leu Gly Leu Asn Phe Gln Pro Asn Lys Lys Tyr Ser Leu Pro Asp Glu  
65 70 75 80

Ser Thr Leu Arg Gln Gln Leu Ser Tyr Gln Phe Pro Tyr Asp Glu Ser  
85 90 95

Lys Pro Phe Pro Lys Asn Ile Trp Gln Thr Trp Lys Val Gly Ile Asp  
100 105 110

Glu Lys Ser Phe Pro Lys Arg Tyr Leu Lys Tyr Gln Gln Thr Trp Glu  
115 120 12